## AMENDMENT

**In the Claims:**

Please amend claims 30, 33, 38, and 39, as shown below.

1-18. **(Cancelled)**

19. (**Withdrawn**) A polypeptide, characterized by

(a) derived from HCV polymerase NS5B having an HCV polymerase activity;

(b) consisting of an amino acid sequence X-Y;

wherein X comprises a consecutive amino acid sequence which is a portion of the NS5B, an N-terminal amino acid of X is the amino acid residue 1 (Ser) of the NS5B, and a C-terminal amino acid of X is an amino acid residue selected from the group consisting of amino acid residues 531 (Lys) to 570 (Arg) of the NS5B;

wherein one or more amino acids in the amino acid sequence of X may be modified, and methionine residues in the amino acid sequence of X may be replaced by selenomethionine residues;

wherein Y comprises a carboxyl group or an amino acid sequence which is not derived from NS5B.

20. (**Withdrawn**) The polypeptide of claim 19, wherein the C-terminal amino acid residue of X is an amino acid residue selected from the group consisting of 536 (Leu) to 552 (Val) of the NS5B.

21. (**Withdrawn**) The polypeptide of claim 20, wherein the C-terminal amino acid residue of X is an amino acid residue selected from the group consisting of 536 (Leu) to 544 (Gln) of the NS5B.

22. (**Withdrawn**) The polypeptide of claim 20, wherein the C-terminal amino acid residue of X is an amino acid residue selected from the group consisting of 531 (Lys) to 544 (Gln) of the NS5B.

23. (**Withdrawn**) The polypeptide of claim 19, wherein methionine residues in the amino acid sequence of X are replaced by selenomethionine residues.

24. (**Withdrawn**) The polypeptide of claim 19, wherein Y is an amino acid sequence not derived from NS5B, and said amino acid sequence is suitable for column purification.

25. (**Withdrawn**) The polypeptide of claim 19, wherein the NS5B comprises an amino acid sequence of SEQ ID NO: 1.

26. (**Withdrawn**) The polypeptide of claim 19, wherein said polypeptide is identified by three-dimensional structural coordinates shown in a table selected from the group consisting of Table 2 and Table 3.

27. (**Withdrawn**) A crystal comprising the polypeptide of claim 19.

28. (**Withdrawn**) A DNA encoding the polypeptide of claim 19.

29. (**Withdrawn**) A method for determining three-dimensional structural

coordinates of a variant of HCV polymerase NS5B by the molecular replacement method using a three-dimensional structure coordinate of said NS5B.

30. **(Currently amended)** A method for identifying a HCV polymerase inhibitor, said method comprising:

determining the complementarity of a test compound with an active site and/or RNA binding cleft of a polypeptide using a three-dimensional structural coordinate of said polypeptide or its part and a three-dimensional structural coordinate of said test compound,

wherein said polypeptide is derived from an NS5B HCV polymerase, has an NS5B HCV polymerase activity, and consists of an amino acid sequence X-Y, wherein X is a consecutive amino acid sequence which is a portion of NS5B, the N-terminal amino acid of X is a serine residue corresponding to amino acid residue 1 of NS5B, and the C-terminal amino acid residue of X is ~~any one of~~ selected from amino acid residues 531 ~~(Lys) to~~, 536, 544, and 570 ~~(Arg)~~ of NS5B; and wherein Y is a carboxyl group or an amino acid sequence which is not derived from NS5B; ~~and wherein one or more amino acids in X may be modified~~, and wherein methionine residues in the amino acid sequence of X may be replaced by selenomethionine residues,

wherein a test compound that is complementary to said active site and/or RNA binding cleft of said polypeptide ~~is a~~ inhibits a HCV polymerase ~~inhibitor~~ by binding to said active site and/or RNA binding cleft of said HCV polymerase.

31. **(Previously presented)** A method for identifying a HCV polymerase inhibitor, which method comprises the steps of:

(a) performing the method of claim 30; and

(b) determining a HCV polymerase-inhibitory activity of said HCV polymerase inhibitor.

32. (**Withdrawn**) The method of claim 29, wherein the three-dimensional structural coordinate of the polypeptide is selected from the group consisting of dimensional structural coordinates shown in a table selected from the group consisting of Table 2 and Table 3.

33. **(Currently amended)** A method for identifying a HCV polymerase inhibitor, which method comprises the steps of:

(a) obtaining a polypeptide which is derived from an NS5B HCV polymerase, has an NS5B HCV polymerase activity, and consists of the amino acid sequence X'-Y, wherein X' is a consecutive amino acid sequence which is a portion of the NS5B, the N-terminal amino acid of X' is a serine residue corresponding to amino acid residue 1 of NS5B, and the C-terminal amino acid residue of X' is ~~any one of~~ selected from amino acid residues 531 ~~(Lys) to~~ , 536, and 544 ~~(Gln)~~ of NS5B; and wherein Y is a carboxyl group or another amino acid sequence which is not derived from NS5B; and wherein ~~one or more amino acids in X' may be modified, and~~ methionine residues in the amino acid sequence of X' may be replaced by selenomethionine residues;

(b) determining the HCV polymerase activity of said polypeptide by reacting said polypeptide obtained in step (a) with a template RNA and substrates in the presence of a test compound;

(c) determining the HCV polymerase activity of said polypeptide by reacting polypeptide obtained in step (a) with a template RNA and substrates in the absence of said test compound; and,

(d) comparing the HCV polymerase activity determined in step (b) with the HCV polymerase activity determined in step (c).

34. (**Withdrawn**) An HCV polymerase inhibitor, identified by the method of claim 30.

35. (**Withdrawn**) An HCV polymerase inhibitor that inhibits the HCV polymerase activity of HCV polymerase NS5B by acting on a boundary between Thumb and Palm domains of NS5B.

36. (**Withdrawn**) The HCV polymerase inhibitor of claim 35, wherein said inhibitor is a compound represented by the formula, Z-Asp-Leu-Ser-Gly-Trp-Phe-Z', wherein *Z* is Leu or a hydrophilic group, and Z' is
Val or a hydrophilic group.

37. **(Canceled)**

38. **(Currently Amended)** The method according to claim 31, wherein the C-terminal amino acid residue of X is selected from the group consisting of amino acid residues ~~531,~~ 536, 544 and 570 of NS5B.

39. **(Currently Amended)** The method according to claim 33, wherein the C-terminal amino acid residue of X' is selected from the group consisting of amino acid residues ~~531, 536,~~ 536 and 544 of NS5B.